

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: MUKHERJEE, RANJAN
- (ii) TITLE OF INVENTION: Human Peroxisome
Proliferator Activated
Receptor γ
- (iii) NUMBER OF SEQUENCES: 2
- (iv) CORRESPONDENCE ADDRESS:
- (A) ADDRESSEE: Lyon & Lyon
(B) STREET: 633 West Fifth Street
Suite 4700
(C) CITY: Los Angeles
(D) STATE: California
(E) COUNTRY: U.S.A.
(F) ZIP: 90071-2066
- (v) COMPUTER READABLE FORM:
- (A) MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
storage
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: IBM P.C. DOS 5.0
(D) SOFTWARE: Word Perfect 5.1
- (vi) CURRENT APPLICATION DATA:
- (A) APPLICATION NUMBER: 08/380,051
(B) FILING DATE: January 30, 1995
(C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
- (A) NAME: Warburg, Richard J.
(B) REGISTRATION NUMBER: 32,327
(C) REFERENCE/DOCKET NUMBER: 210/100
- (ix) TELECOMMUNICATION INFORMATION:
- (A) TELEPHONE: (213) 489-1600
(B) TELEFAX: (213) 955-0440
(C) TELEX: 67-3510

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(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1641 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

GAATTCCGGA CCCTCAACAC CACTCCCTCT TAGCCAATAT TGTGCCTATT 50
 GCCATACTAG TCTTTGCGCC TCGAAGCAG CGGTGGCCTA GCCCTACTAG 100
 TCTCAATCTC CAACATATAT CGGCCTAGAC TACGTACATA ACCTAAACCT 150
 ACTCCAATGC TAAAACTAAT CGTCCCTTTT CTCAAACGAG AGTCAGCCTT 200
 TAACGAAATG ACCATGGTTG ACACAGAGAT GCCATTCTGG CCCACCAACT 250
 TTGGGATCAG CTCCGTGGAT CTCTCCGTAA TGGAAGACCA CTCCCCTCC 300
 TTTGATATCA AGCCCTTCAC TACTGTTGAC TTCTCCAGCA TTTCTACTCC 350
 ACATTACGAA GACATTCCAT TCACAAGAAC AGATCCAGTG GTTGCAGATT 400
 ACAAGTATGA CCTGAAACTT CAAGAGTACC AAAGTGCAAT CAAAGTGGAG 450
 CCTGCATCTC CACCTTATTA TTCTGAGAAG ACTCAGCTCT ACAATAAGCC 500
 TCATGAAGAG CCTTCCAACCT CCCTCATGGC AATTGAATGT CGTGTCTGTG 550
 GAGATAAAGC TTCTGGATTT CACTATGGAG TTCATGCTTG TGAAGGATGC 600
 AAGGGTTTCT TCCGGAGAAC AATCAGATTG AAGCTTATCT ATGACAGATG 650
 TGATCTTAAC TGTCGGATCC ACAAAAAAAG TAGAAATAAA TGTCAGTACT 700
 GTCGGTTTCA GAAATGCCTT GCAGTGGGGA TGTCTCATAA TGCCATCAGG 750
 TTTGGGCGGA TGCCACAGGC CGAGAAGGAG AAGCTGTTGG CGGAGATCTC 800
 CAGTGATATC GACCAGCTGA ATCCAGAGTC CGCTGACCTC CGGGCCCTGG 850
 CAAAACATTT GTATGACTCA TACATAAAGT CCTTCCCGCT GACCAAAGCA 900
 AAGGCGAGGG CGATCTTGAC AGGAAAGACA ACAGACAAAT CACCATTCGT 950
 TATCTATGAC ATGAATTCCT TAATGATGGG AGAAGATAAA ATCAAGTTCA 1000
 AACACATCAC CCCCTGCAG GAGCAGAGCA AAGAGGTGGC CATCCGCATC 1050
 TTTCAGGGCT GCCAGTTTCG CTCCGTGGAG GCTGTGCAGG AGATCACAGA 1100
 GTATGCCAAA AGCATTCCTG GTTTTGTAAG TCTTGACTTG AACGACCAAG 1150

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(2) INFORMATION FOR SEQ ID NO: 2:

(A) LENGTH: 494 amino acids
(B) TYPE: amino acid
(C) STRANDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION : SEQ ID NO: 2

Met	Leu	Lys	Leu	Ile 5	Val	Pro	Phe	Leu	Lys 10	Arg	Glu	Ser	Ala	Phe 15
Asn	Glu	Met	Thr	Met 20	Val	Asp	Thr	Glu	Met 25	Pro	Phe	Trp	Pro	Thr 30
Asn	Phe	Gly	Ile	Ser 35	Ser	Val	Asp	Leu	Ser 40	Val	Met	Glu	Asp	His 45
Ser	His	Ser	Phe	Asp 50	Ile	Lys	Pro	Phe	Thr 55	Thr	Val	Asp	Phe	Ser 60
Ser	Ile	Ser	Thr	Pro 65	His	Tyr	Glu	Asp	Ile 70	Pro	Phe	Thr	Arg	Thr 75
Asp	Pro	Val	Val	Ala 80	Asp	Tyr	Lys	Tyr	Asp 85	Leu	Lys	Leu	Gln	Glu 90

Tyr Gln Ser Ala Ile Lys Val Glu Pro Ala Ser Pro Pro Tyr Tyr
 95 100 105
 Ser Glu Lys Thr Gln Leu Tyr Asn Lys Pro His Glu Glu Pro Ser
 110 115 120
 Asn Ser Leu Met Ala Ile Glu Cys Arg Val Cys Gly Asp Lys Ala
 125 130 135
 Ser Gly Phe His Tyr Gly Val His Ala Cys Glu Gly Cys Lys Gly
 140 145 150
 Phe Phe Arg Arg Thr Ile Arg Leu Lys Leu Ile Tyr Asp Arg Cys
 155 160 165
 Asp Leu Asn Cys Arg Ile His Lys Lys Ser Arg Asn Lys Cys Gln
 170 175 180
 Tyr Cys Arg Phe Gln Lys Cys Leu Ala Val Gly Met Ser His Asn
 185 190 195
 Ala Ile Arg Phe Gly Arg Met Pro Gln Ala Glu Lys Glu Lys Leu
 200 205 210
 Leu Ala Glu Ile Ser Ser Asp Ile Asp Gln Leu Asn Pro Glu Ser
 215 220 225
 Ala Asp Leu Arg Ala Leu Ala Lys His Leu Tyr Asp Ser Tyr Ile
 230 235 240
 Lys Ser Phe Pro Leu Thr Lys Ala Lys Ala Arg Ala Ile Leu Thr
 245 250 255
 Gly Lys Thr Thr Asp Lys Ser Pro Phe Val Ile Tyr Asp Met Asn
 260 265 270
 Ser Leu Met Met Gly Glu Asp Lys Ile Lys Phe Lys His Ile Thr
 275 280 285
 Pro Leu Gln Glu Gln Ser Lys Glu Val Ala Ile Arg Ile Phe Gln
 290 295 300
 Gly Cys Gln Phe Arg Ser Val Glu Ala Val Gln Glu Ile Thr Glu
 305 310 315
 Tyr Ala Lys Ser Ile Pro Gly Phe Val Asn Leu Asp Leu Asn Asp
 320 325 330
 Gln Val Thr Leu Leu Lys Tyr Gly Val His Glu Ile Ile Tyr Thr
 335 340 345
 Met Leu Ala Ser Leu Met Asn Lys Asp Gly Val Leu Ile Ser Glu
 350 355 360
 Gly Gln Gly Phe Met Thr Arg Glu Phe Leu Lys Ser Leu Arg Lys
 365 370 375

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Pro	Phe	Gly	Asp	Phe	Met	Glu	Pro	Lys	Phe	Glu	Phe	Ala	Val	Lys
				380					385					390
Phe	Asn	Ala	Leu	Glu	Leu	Asp	Asp	Ser	Asp	Leu	Ala	Ile	Phe	Ile
				395					400					405
Ala	Val	Ile	Ile	Leu	Ser	Gly	Asp	Arg	Pro	Gly	Leu	Leu	Asn	Val
				410					415					420
Lys	Pro	Ile	Glu	Asp	Ile	Gln	Asp	Asn	Leu	Leu	Gln	Ala	Leu	Glu
				425					430					435
Leu	Gln	Leu	Lys	Leu	Asn	His	Pro	Glu	Ser	Ser	Gln	Leu	Phe	Ala
				440					445					450
Lys	Leu	Leu	Gln	Lys	Met	Thr	Asp	Leu	Arg	Gln	Ile	Val	Thr	Glu
				455					460					465
His	Val	Gln	Leu	Leu	Gln	Val	Ile	Lys	Lys	Thr	Glu	Thr	Asp	Met
				470					475					480
Ser	Leu	His	Pro	Leu	Leu	Gln	Glu	Ile	Tyr	Lys	Asp	Leu	Tyr	
				485					490					

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